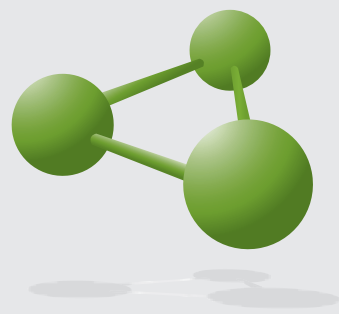


# 3DM'S PATENT ANALYSIS SUITE BY BIO-PRODUCT

1. 3DM introduction
2. 3DM's patent analysis suite



# 1. 3DM INTRODUCTION





The 3D-numbers synchronize all sequences and allows for the transfer of mutation data from patents to any target protein.

27  
27  
27  
27  
27  
27

In the first step of the generation of a 3DM superfamily platform 3DM superimposes all available structures for the protein family and groups the structures into subfamilies. From these groups one template structure is selected that is used to align sequences for which no structures are available thereby forming subfamily alignments. Here 140 of such template structures are shown for the kinase protein family. The resulting 140 subfamilies are combined into one large superfamily alignment. In total the alignment for the kinases contains over 114.000 WT sequences. A 3D-numbering scheme, in which all structural equivalent residues get the same number (e.g. are in the same column in the alignment), is applied to all sequences, all structures, and to the alignments. Here, the labels of the purple residues located at 3D-position 27 are shown. The 3D-numbers synchronize all sequences and structures.



Dashboard

# Alignment (structures excluded)

3DM System

Start

Alignment

Alignment statistics

Correlated mutations

Visualize

Phylogeny

Panel design

Patents

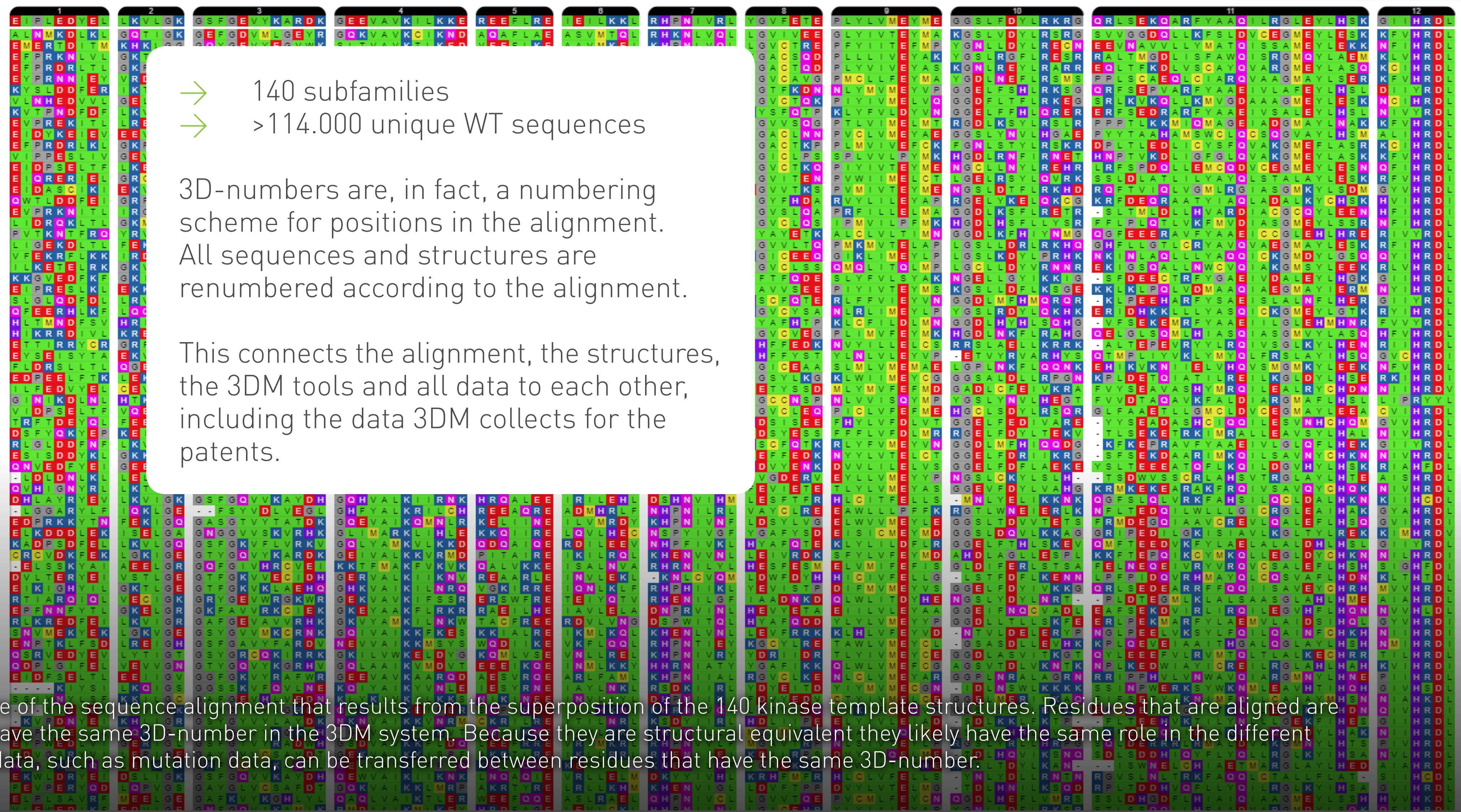
Proteins

Search

System

Overall consensus

- 1BYGA
- 3KFAA
- 2X2LA
- 3CLYA
- 1LUFA
- 1RDOE
- 3CBLA
- 106LA
- 1P4OA
- 2EVAA
- 2XIRA
- 3F66B
- 3GENA
- 1MP8A
- 200LA
- 2VGPB
- 2YFXA
- 3BRBA
- 3C4ZA
- 3EORA
- 3LXPA
- 3POZA
- 3RCJA
- 2SRCA
- 3A8XB
- 3LXLA
- 3PVUA
- 3V5OB
- 2RKUA
- 1J1BB
- 1XBBA
- 3A7IA
- 3C0IA
- 3KMUA
- 3MIYA
- 3KK8A
- 1PHKA
- 1XJDA
- 2WEIA
- 3BHYA
- 3G2FA
- 3IECA
- 3KVWA
- 2BUJA
- 2J0IA
- 3EOCA
- 3G51A
- 3MI9A
- 1TKIA
- 2EU9A
- 2H6DA
- 3HMMMA
- 3LM5A
- 3TKUA
- 4AAA
- 1U5RB
- 2W5AA
- 2X7FA
- 3DTCA
- 3HMPA
- 3N3YA
- 3P66B
- 3S00B
- 2VX3B
- 3ZYAA
- 3ZZWB
- 3F10B



- 140 subfamilies
- >114.000 unique WT sequences

3D-numbers are, in fact, a numbering scheme for positions in the alignment. All sequences and structures are renumbered according to the alignment.

This connects the alignment, the structures, the 3DM tools and all data to each other, including the data 3DM collects for the patents.

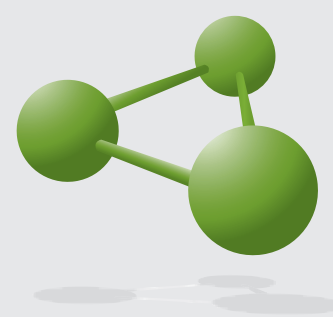
This is a zoomed out picture of the sequence alignment that results from the superposition of the 140 kinase template structures. Residues that are aligned are structural equivalent and have the same 3D-number in the 3DM system. Because they are structural equivalent they likely have the same role in the different proteins. This means that data, such as mutation data, can be transferred between residues that have the same 3D-number.

# MANY DIFFERENT DATA TYPES ARE COLLECTED FOR ALL SEQUENCES IN THESE LARGE ALIGNMENTS

- **Mutation data**  
From literature: 264.605...  
From patents: 1.683 mutations have been extracted from claimes.
- **Structure data**  
PPI, ligand contacts, bridges, solvent accessibility, flexibility/RMSD, ...
- **Alignment data**  
Conservation, correlated mutations, family specific residues, ...
- **SNP data**  
SNP databases, genome sequencing projects
- **Data- and tool integration**  
All data are stored connected to the 3D numbering scheme and thus to the alignment, to the structures, all 3DM tools, and each other.

3DM collects many different data types from all kinds of sources for all the 114.000 proteins that are available in this kinase protein family. These are all stored connected to the 3D-numbers. This connects all data to each other making it possible to make very complex queries. For example, it now takes a couple of seconds to find out if mutations reported in the literature that cause effects on specificity are more often found at positions that show a correlated mutation behavior in the alignment. Manually such comparisons can easily be a year work.

## 2. 3DM'S PATENT ANALYSIS SUITE



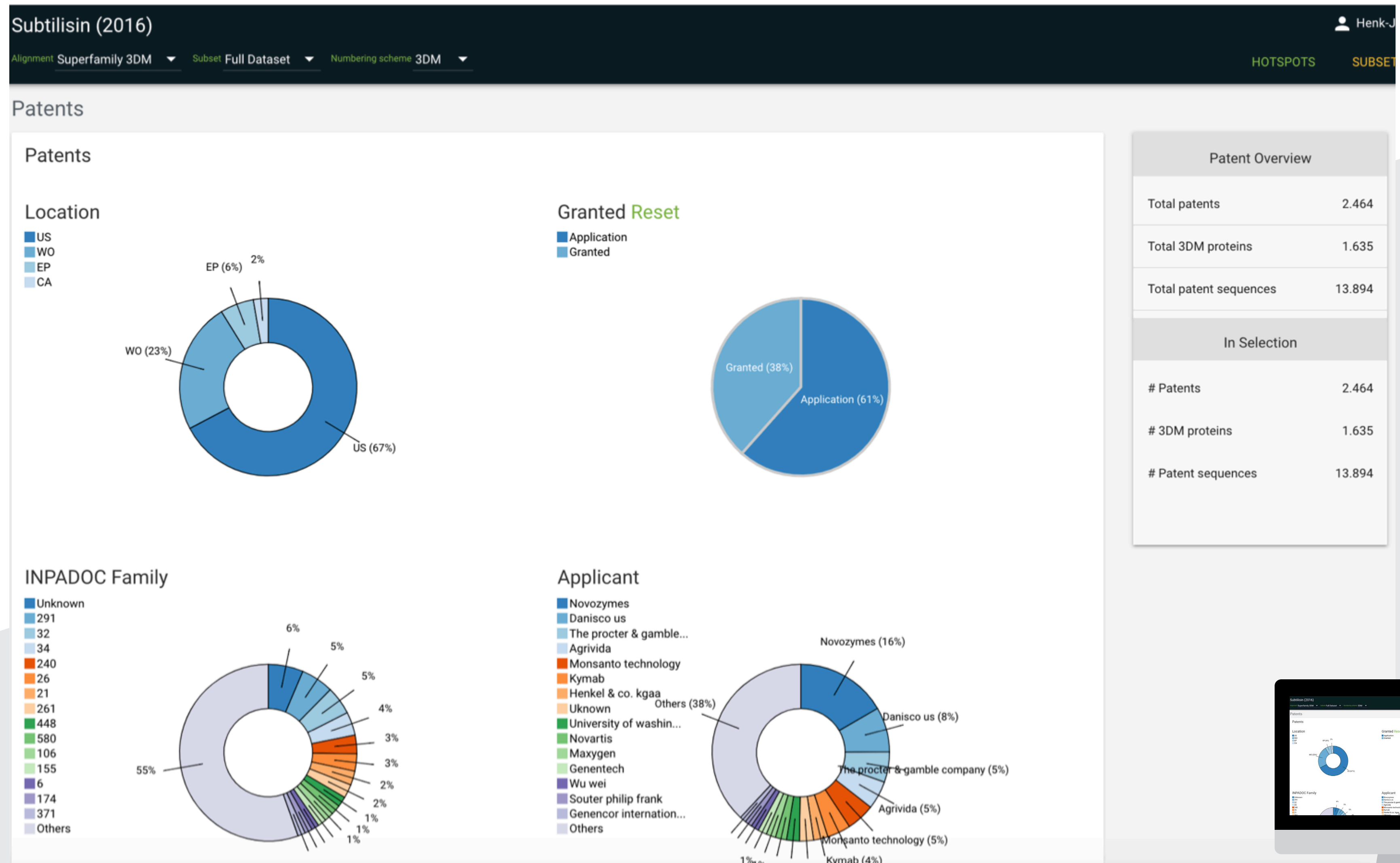
# PATENT DATA EXTRACTION

## → **Collection of patents for complete protein families**

- › Claimed and mentioned sequences
- › Claimed sequence spaces
- › Claimed mutations › Patent family information
- › Bibliographic data:
  - I Priority, filing and publication dates
  - II Applicants
  - III Titles & abstracts
  - IV Many others...
- › Inventors
- › Many other data types

3DM collects the patents for complete protein superfamilies by combining complex patent sequence searches with a smart patent family search. For important heavily patented protein families, such as the kinase protein family or the antibody protein family, 3DM collects many (7.944 and 44.859 respectively) patents. From these patents many different data types are extracted, such as claimed sequences and claimed mutations. For the kinase and antibody protein families 3DM extracted 131.578 and 703.356 sequences, and 1.683 and 5.180 mutations, respectively.

# DIFFERENT ONLINE SELECTION TOOLS FOR ANALYSIS OF THE PATENTS



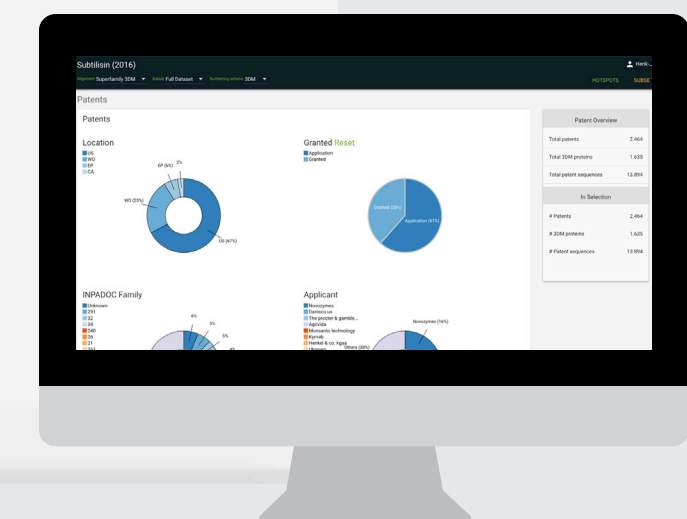
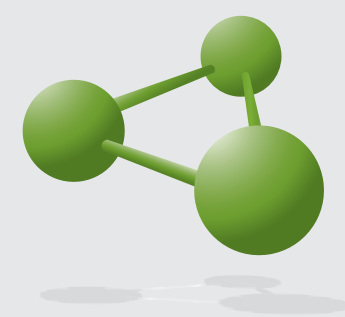
### Patent Overview

Total patents	2.464
Total 3DM proteins	1.635
Total patent sequences	13.894

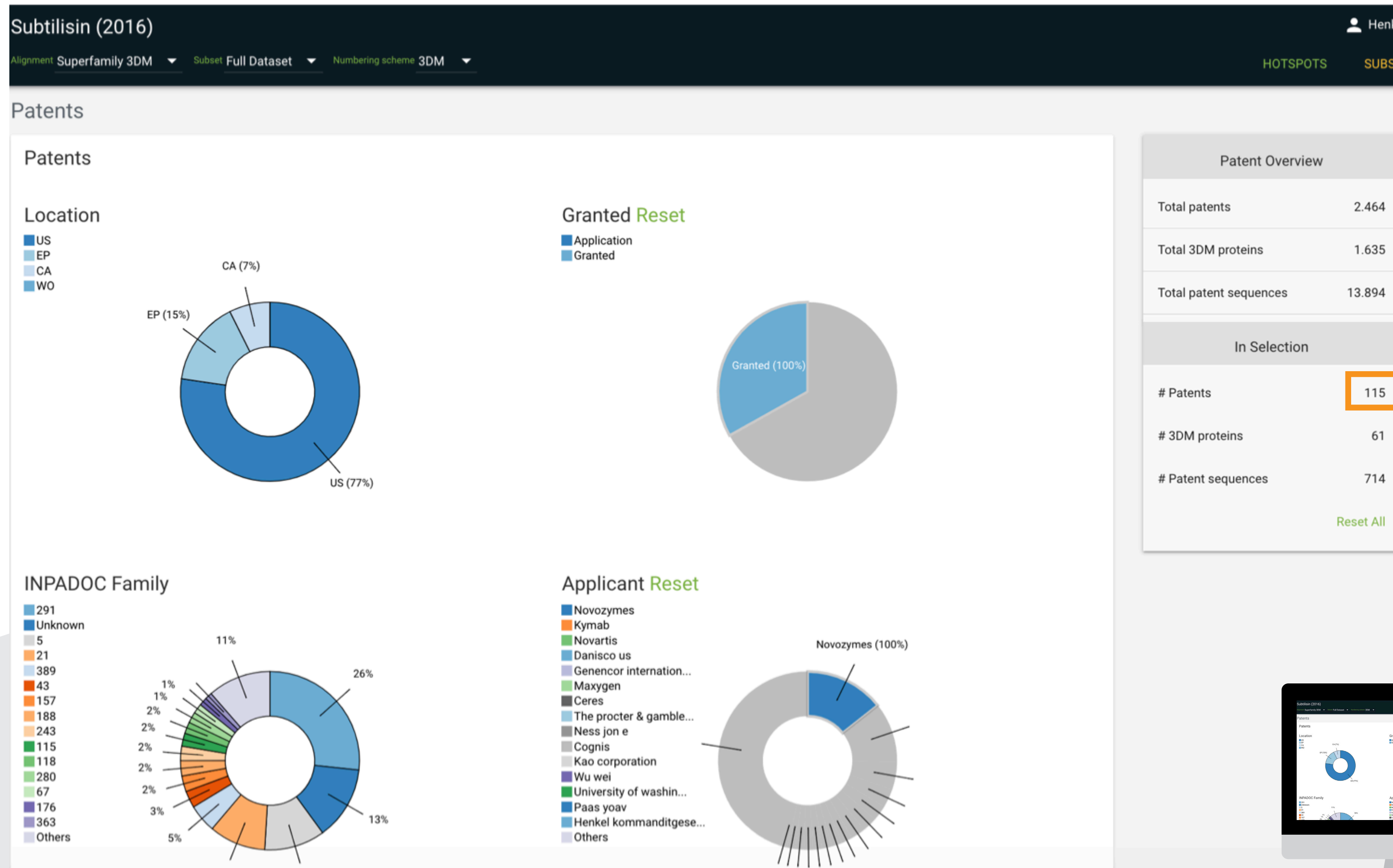
### In Selection

# Patents	2.464
# 3DM proteins	1.635
# Patent sequences	13.894

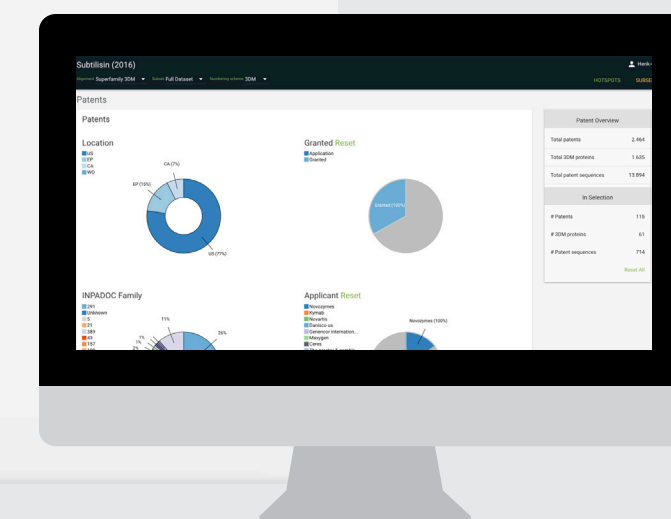
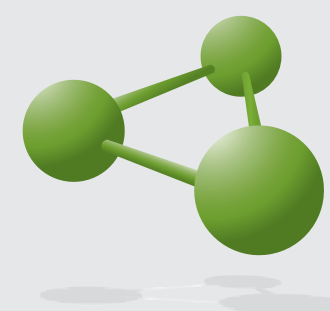




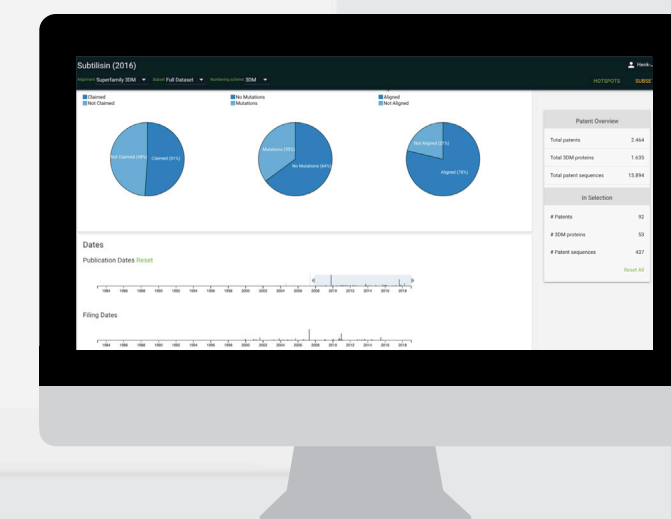
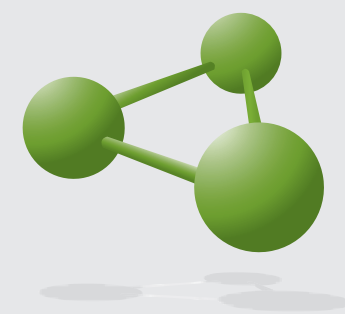
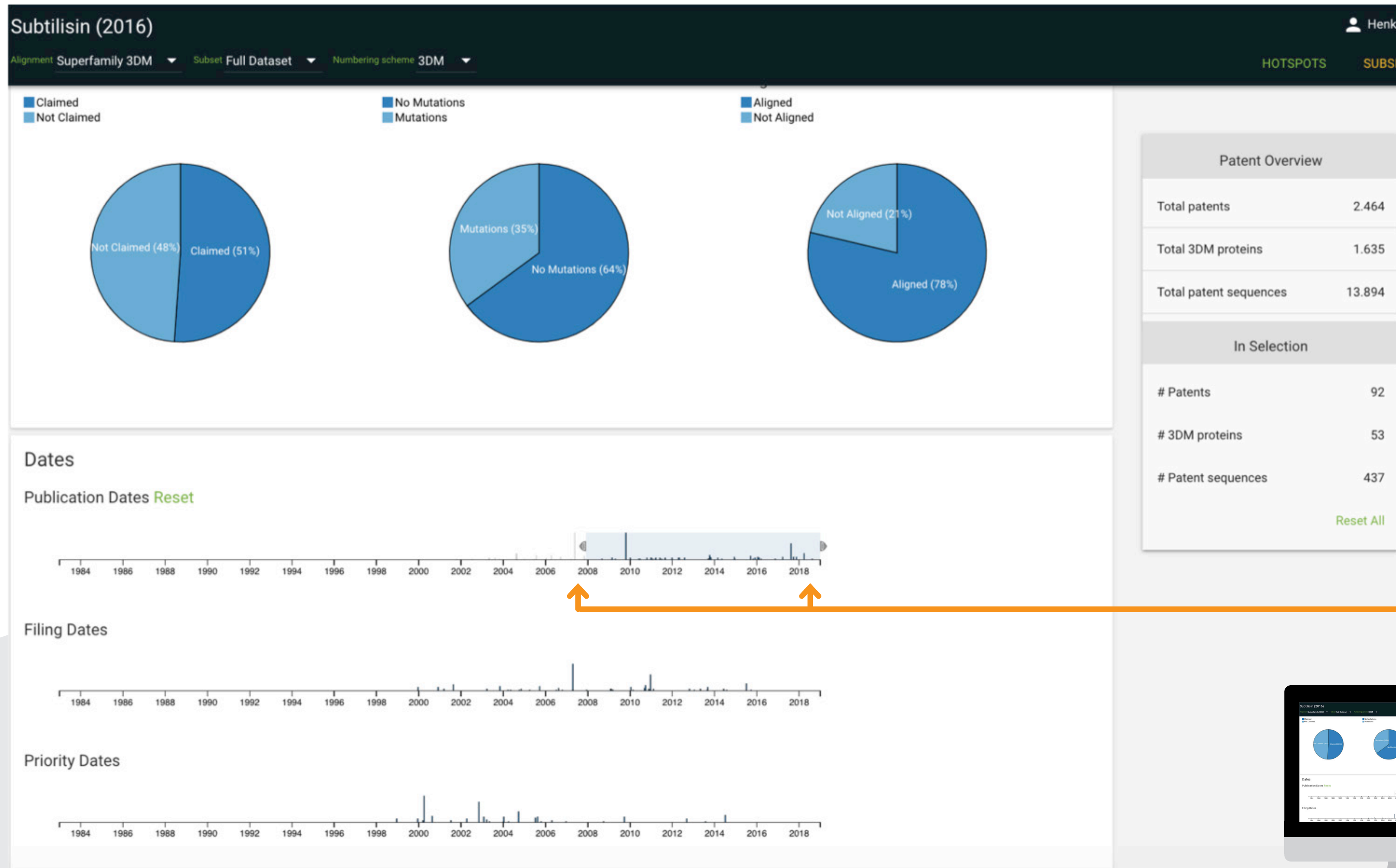
# DIFFERENT ONLINE SELECTION TOOLS FOR ANALYSIS OF THE PATENTS



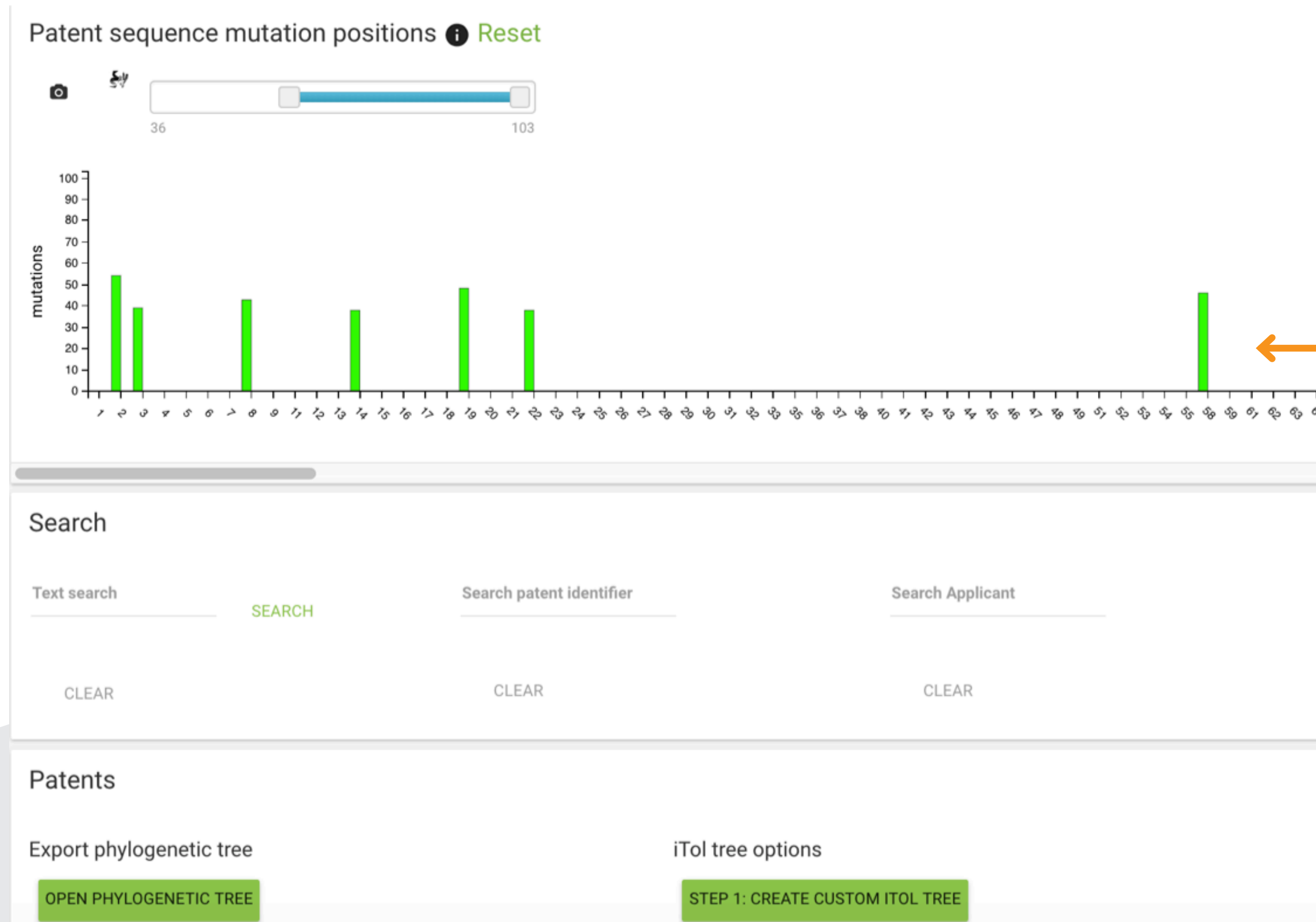
Here all granted patents from Novozymes are selected. Novozymes has 115 granted patents in this protein family.



# DIFFERENT ONLINE SELECTION TOOLS FOR ANALYSIS OF THE PATENTS



# DIFFERENT VISUALISATION OPTIONS



Patent Overview

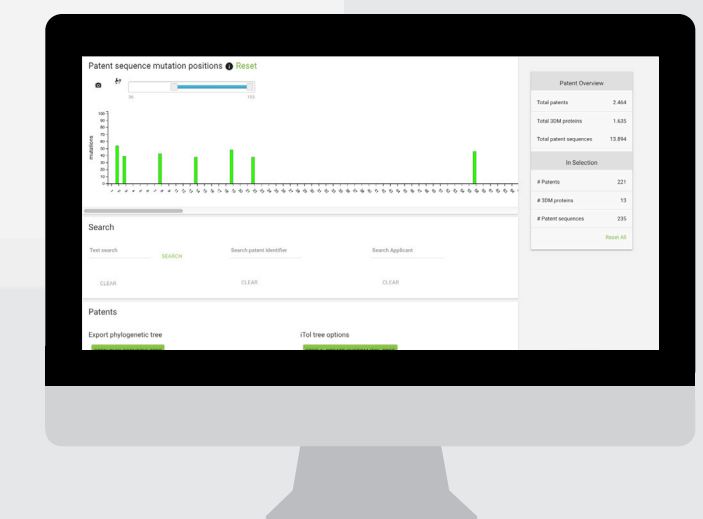
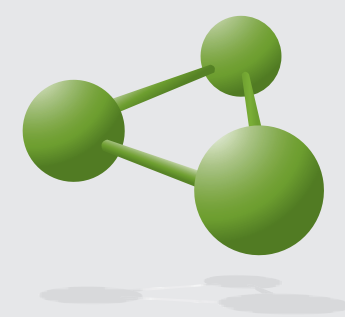
Total patents	2.464
Total 3DM proteins	1.635
Total patent sequences	13.894

In Selection

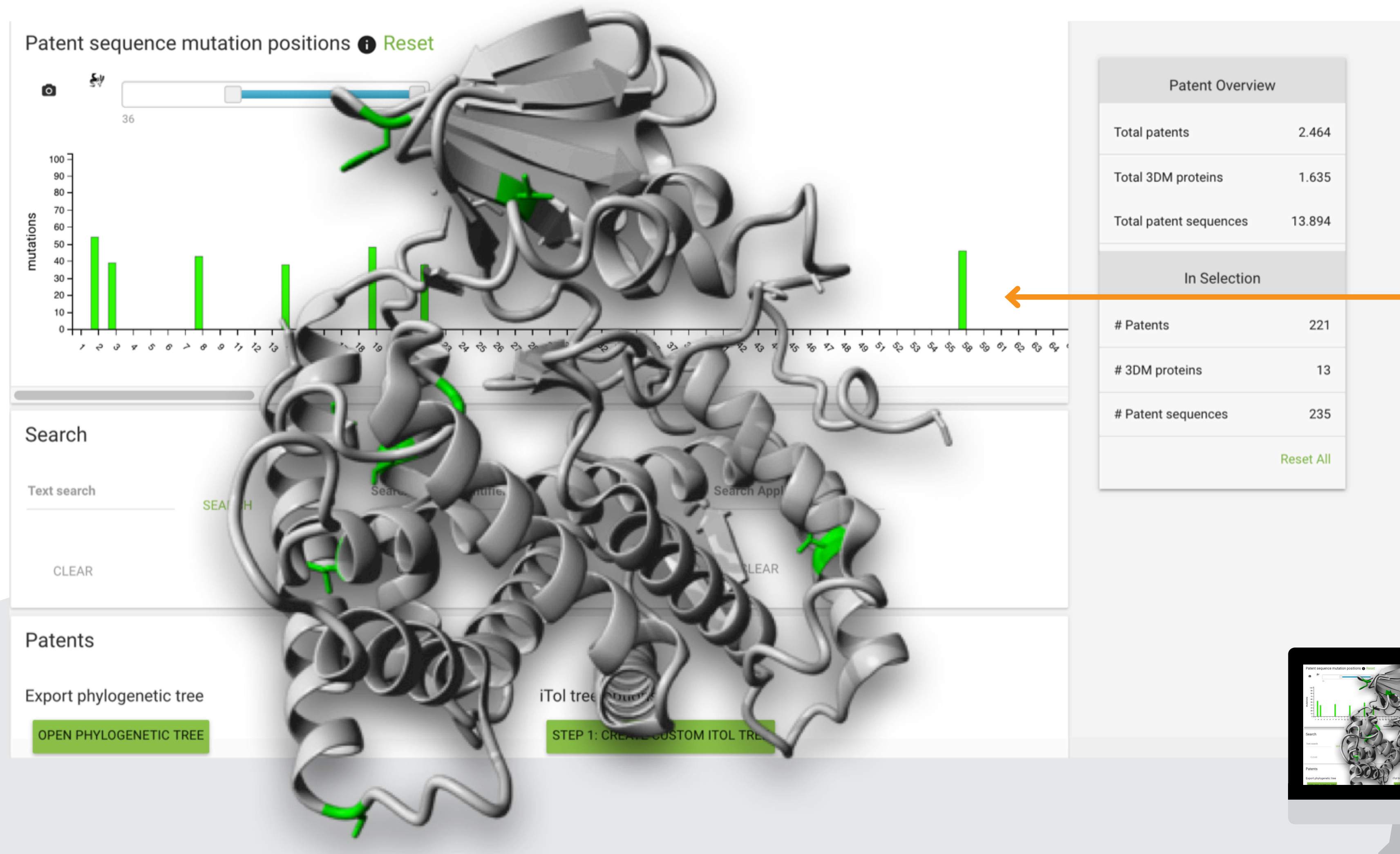
# Patents	221
# 3DM proteins	13
# Patent sequences	235

[Reset All](#)

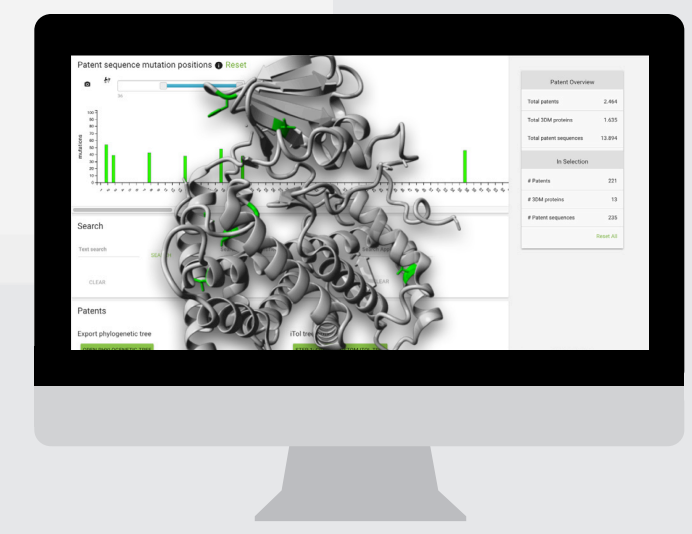
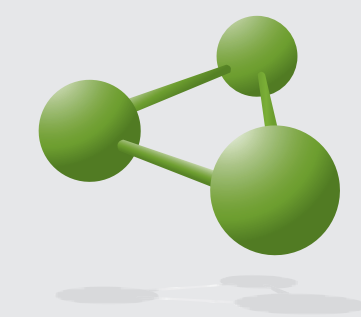
Interactive histogram visualising mutations claimed by novozymes.



# MANY OPTIONS FOR VISUALIZING PATENT DATA



The selected mutation data can instantly be visualized in any available protein structure or homology model.



# MANY OPTIONS FOR VISUALIZING PATENT DATA

The patented sequences can instantly be visualized in the phylogenetic tree of the superfamily for FTO analysis.

Patent sequence mutation p

36

mutations

100  
90  
80  
70  
60  
50  
40  
30  
20  
10  
0

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Search

Text search SEARCH

CLEAR

Patents

Export phylogenetic tree

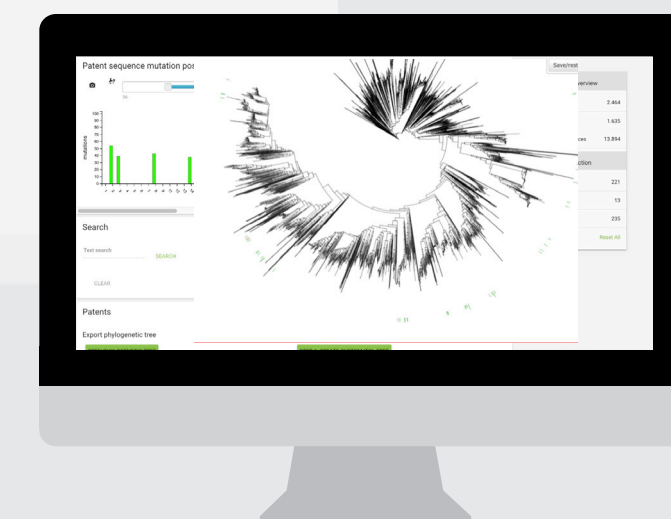
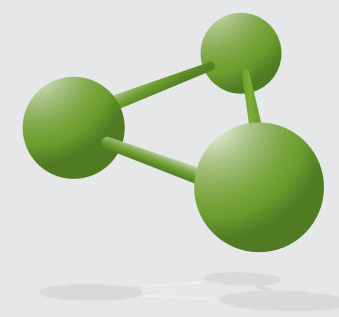
OPEN PHYLOGENETIC TREE

Save/resto

view

2.464
1.635
13.894
ion
221
13
235
Reset All

STEP 1: CREATE CUSTOM ITOL TREE



# SUMMARY OF THE SELECTED PATENTS IS PROVIDED

Link to interactive analysis tool for each patent

Patent List

[DOWNLOAD PATENT SEQUENCES](#)

First Previous **1** 2 Next Last

92 patents in selection

[Family:115 - US7951573 B2](#) [External link](#)

**Subtilases**

Applicant: Novozymes Publication type: Granted Sequences: 8

Published: 31/05/2011  
Filed: 18/11/2010  
Priority: 16/08/2005

**Abstract**

The present invention relates to novel subtilases from wild-type strains of Bacillus, especially the Bacillus strains ZI344, EP655, P203, EP63, ZI120, ZI130, ZI1342 and ZI140, and to methods of construction and production of these proteases. Further, the present invention relates to use of the claimed subtilases in detergents, such as a laundry detergent or an automatic dishwashing detergent.

**Patented sequences** [Show more...](#)

SEQ ID	Claimed	Mutations	Linked protein in 3DM	Similarity	Claimed seq. space
2	Not Claimed	0	S5VEF0	81.87%	
4	Not Claimed	0	S5VEF0	82.93%	
6	Not Claimed	0	S5VEF0	82.93%	

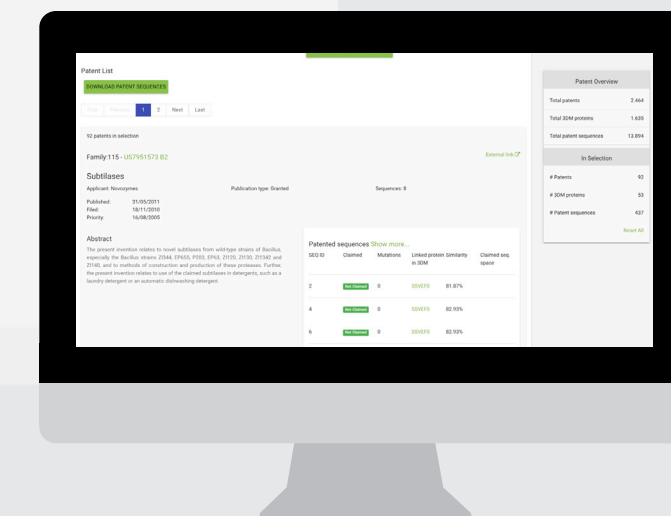
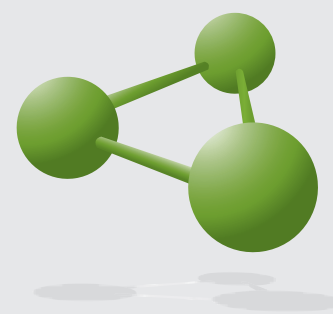
**Patent Overview**

Total patents	2.464
Total 3DM proteins	1.635
Total patent sequences	13.894

**In Selection**

# Patents	92
# 3DM proteins	53
# Patent sequences	437

[Reset All](#)



# INTERACTIVE TOOL FOR ANALYSIS A PATENT SHOWING CLAIMED SEQUENCES AND MUTATIONS

Subtilisin (2016)
Henk-Jan Joosten

Alignment Superfamily 3DM
Subset Full Dataset
Numbering scheme 3DM
HOTSPOTS SUBSETS

patent US9133423 B2

### SUBTILASE VARIANTS

Applicant: NOVOZYMES A/S, [External link](#)

**Abstract**

The present invention relates to novel subtilase variants exhibiting improvements relative to the parent subtilase in one or more properties including: wash performance, thermal stability, storage stability or catalytic activity. The variants of the invention are suitable for use in e.g., cleaning or detergent compositions, such as laundry detergent compositions and dish wash compositions, including automatic dish wash compositions.

**Type:** Granted  
**Published:** 15/09/2015  
**Filed:** 15/01/2010  
**Priority:** 08/07/2005

### Simple family members

[US20100120091 A1](#)

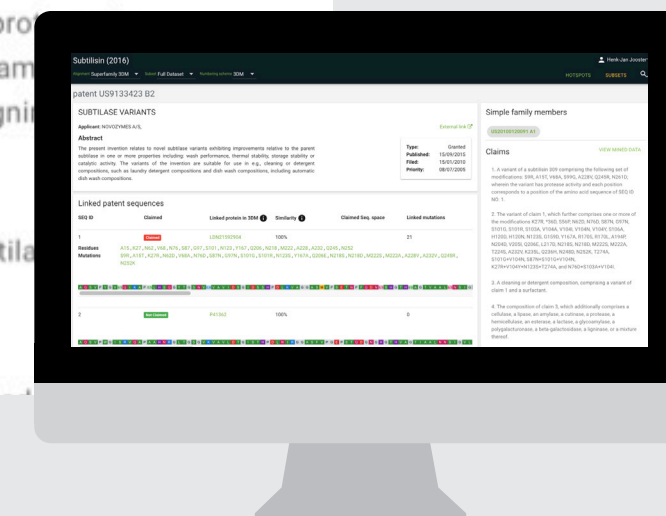
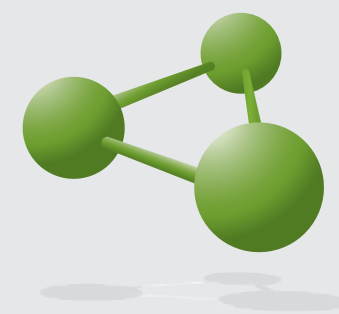
### Claims

[VIEW MINED DATA](#)

1. A variant of a subtilisin 309 comprising the following set of modifications: S9R, A15T, V68A, S99G, A228V, Q245R, N261D; wherein the variant has protease activity and each position corresponds to a position of the amino acid sequence of SEQ ID NO: 1.
2. The variant of claim 1, which further comprises one or more of the modifications K27R, \*36D, S56P, N62D, N76D, S87N, G97N, S101G, S101R, S103A, V104A, V104I, V104N, V104Y, S106A, H120D, H120N, N123S, G159D, Y167A, R170S, R170L, A194P, N204D, V205I, Q206E, L217D, N218S, N218D, M222S, M222A, T224S, A232V, K235L, Q236H, N248D, N252K, T274A, S101G+V104N, S87N+S101G+V104N, K27R+V104Y+N123S+T274A, and N76D+S103A+V104I.
3. A cleaning or detergent composition, comprising a variant of claim 1 and a surfactant.
4. The composition of claim 3, which additionally comprises a cellulase, a lipase, an amylase, a cutinase, a pectinase, a hemicellulase, an esterase, a lactase, a glycoamylase, a polygalacturonase, a beta-galactosidase, a ligninase or thereof.
5. An isolated DNA sequence encoding a subtilase variant of claim 1.

### Linked patent sequences

SEQ ID	Claimed	Linked protein in 3DM	Similarity	Claimed Seq. space	Linked mutations
1	Claimed	LDN21592904	100%		21
<b>Residues</b>	A15, K27, N62, V68, N76, S87, G97, S101, N123, Y167, Q206, N218, M222, A228, A232, Q245, N252				
<b>Mutations</b>	S9R, A15T, K27R, N62D, V68A, N76D, S87N, G97N, S101G, S101R, N123S, Y167A, Q206E, N218S, N218D, M222S, M222A, A228V, A232V, Q245R, N252K				
<div style="font-family: monospace; font-size: 0.8em; color: #2c3e50;"> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">Q</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">P</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">Y</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">Q</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">I</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">K</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">P</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">L</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">H</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">Q</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">Y</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">T</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">N</span> <span style="background-color: #2c3e50; 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color: white; padding: 2px;">H</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">P</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">D</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">L</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">K</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">M</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; 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2	Not Claimed	P41362	100%		0
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color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">P</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">H</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">N</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">R</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">L</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">T</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">K</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">L</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">D</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">T</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">I</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">T</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">H</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">P</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">D</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">L</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">N</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">I</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">R</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">F</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">P</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">E</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">P</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">T</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">Q</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">D</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">N</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">H</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">T</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">H</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">T</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">I</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">A</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">L</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">N</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">N</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">S</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">I</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">G</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">V</span> <span style="background-color: #2c3e50; color: white; padding: 2px;">L</span> </div>					



# MOVING MOUSE OVER DATA WILL HIGHLIGHT THE CLAIM IN WHICH 3DM FOUND THE SELECTED DATA POINT

Subtilisin (2016) Henk-Jan Joosten

Alignment Superfamily 3DM Subset Full Dataset Numbering scheme 3DM HOTSPOTS SUBSETS

patent US9133423 B2

### SUBTILASE VARIANTS

Applicant: NOVOZYMES A/S External link

**Abstract**

The present invention relates to novel subtilase variants exhibiting improvements relative to the parent subtilase in one or more properties including: wash performance, thermal stability, storage stability or catalytic activity. The variants of the invention are suitable for use in e.g., cleaning or detergent compositions, such as laundry detergent compositions and dish wash compositions, including automatic dish wash compositions.

**Type:** Granted

**Published:** 15/09/2015

**Filed:** 15/01/2010

**Priority:** 08/07/2005

### Simple family members

US20100120091 A1 VIEW MINED DATA

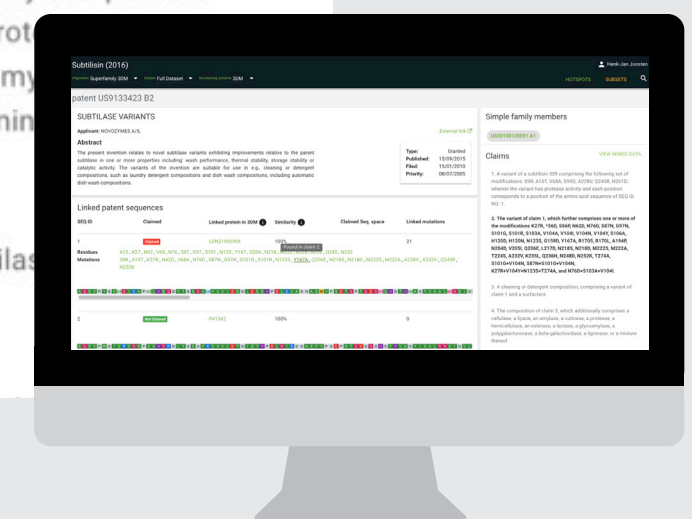
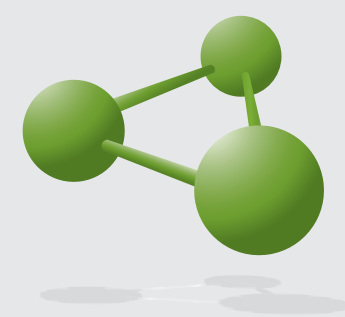
### Claims

1. A variant of a subtilisin 309 comprising the following set of modifications: S9R, A15T, V68A, S99G, A228V, Q245R, N261D; wherein the variant has protease activity and each position corresponds to a position of the amino acid sequence of SEQ ID NO: 1.
2. The variant of claim 1, which further comprises one or more of the modifications K27R, \*36D, S56P, N62D, N76D, S87N, G97N, S101G, S101R, S103A, V104A, V104I, V104N, V104Y, S106A, H120D, H120N, N123S, G159D, Y167A, R170S, R170L, A194P, N204D, V205I, Q206E, L217D, N218S, N218D, M222S, M222A, T224S, A232V, K235L, Q236H, N248D, N252K, T274A, S101G+V104N, S87N+S101G+V104N, K27R+V104Y+N123S+T274A, and N76D+S103A+V104I.
3. A cleaning or detergent composition, comprising a variant of claim 1 and a surfactant.
4. The composition of claim 3, which additionally comprises a cellulase, a lipase, an amylase, a cutinase, a protease, a hemicellulase, an esterase, a lactase, a glycoamylase, a polygalacturonase, a beta-galactosidase, a ligninase or any combination thereof.
5. An isolated DNA sequence encoding a subtilase variant of claim 1.

### Linked patent sequences

SEQ ID	Claimed	Linked protein in 3DM	Similarity	Claimed Seq. space	Linked mutations
1	Claimed	LDN21592904	100% <small>Found in claim 2</small>		21
<p><b>Residues</b> A15, K27, N62, V68, N76, S87, G97, S101, N123, Y167, Q206, N218, M222, A228, A232, Q245, N252</p> <p><b>Mutations</b> S9R, A15T, K27R, N62D, V68A, N76D, S87N, G97N, S101G, S101R, N123S, <u>Y167A</u>, K205E, N218S, N218D, M222S, M222A, T224S, A232V, K235L, Q236H, N248D, N252K, T274A, N252K</p> <p>A Q S V P Y G V I S Q I K A P A L H S Q G Y T G S N V K V A V I D S G I D S S H P D L K V A G G A S M V P S E T N P F Q D N I N S H G T H V A G T V A A L N N S I G</p>					
2	Not Claimed	P41362	100%		0
<p>A Q S V P W G I S R V Q A P A A H N R G L T G S G V K V A V L D T G I S T H P D L N I R G G A S F V P G E P S T O D G N G H G T H V A G T I A A L N N S I G V L</p>					

Interactively analyse claimed sequences and mutations in a patent.





# TOOL FOR PROJECTING PATENT DATA ON A CUSTOM TARGET SEQUENCE

GENERAL SEQUENCE SEQUENCE PROJECTION (BETA)

Sequence

QQTVPWGITRVQAPAVHNRGITGSGVRVAILDGISAHSDLNIRGGASFVPGEPTTADLNHGHGTHVAGTVAALNNSIGVI 80  
GVAPNAELYAVKVLGANGSGSVSGIAQGLEWAATNNMHIANMSLGSDFPSSTLERAVNYATSRDVLVIAATGNNGSGSVG 160  
YPARYANAMAVGATDQNNRRANFSQYGTGIDIVAPGVNVQSTYPGNRYVSMNGTSMATPHVAGAAALVKQRYPSWNATQI 240  
RNHLKNTATNLGNSSQFGSGLVNAEAATR

Visualizations

- Core regions
- Patent mutations BLAST

Similarity (%) 30

1. Custom sequences can be uploaded to 3DM
2. 3DM connects the sequence to the alignment
3. Blast searches can be performed against the patented sequences
4. Patented mutations are visualized in the target sequence (purple residues)

Here the cut-off was set on 30% sequence identity. So, all mutations claimed in sequences that are >30% identical are plotted on the target sequence.

This is a screenshot of 3DM's sequence projection tool. This tool allows for the visualization of data from homologues sequences directly on your target protein. This feature is unique to 3DM and makes 3DM such a powerful tool. As different homologues proteins have different numbering schemes this is very difficult and time consuming to do manually. For instance, if you are interested in a certain amino acid in your target, it is very difficult to find all patents that claim a mutation at that specific position. The 3D-numbering scheme synchronizes the patented sequences to any protein target making such complex searches very easy.

# CLICKING ON A PURPLE RESIDUE PROVIDES A LIST OF PATENTS THAT HAVE CLAIMED MUTATIONS AT THE SELECTED POSITION

GENERAL SEQUENCE SEQUENCE PROJECTION (BETA)

Sequence

QQTVPWGI TRVQAPAVHNRGI TGSGVRVA ILDSGI SAHSDLNIRGGASFVPGEPTTADLNHGHTHVAGTVAALNNSIGVI 80  
GVAPNAELYAVKVLGANGSGSVSGIAQGLEWAATNNMHI ANMSLGSDFPSSTLERAVNYATSRDVLVIAATGNNGSGSVG 160  
YPARYANAMAVGATDQNNRRANFSQYGTGIDIVAPGVNVQSTYPGNRYVSMNGTSMATPHVAGAAALVKQRYPSWNATQI 240  
RNHLKNTATNLGNSSQFGSGLVNAEAATR

**V** 199 Valine (Val)  
Alignment position: 191 (aligned in core region)

STORAGE-STABLE LIQUID DISHWASHING DETERGENT CONTAINING PROTEASE AND AMYLASE **2 Patents in simple family**

In a liquid dishwashing detergent comprising a protease and amylase, storage stability is to be improved. This is achieved through the use of a protease comprising an amino acid sequence having at least 70% identity over its total length with the amino acid sequence specified in SEQ ID NO. 1 and having, in the listing according to SEQ ID NO. 1, the L211D amino acid substitution in combination with at least two further amino acid substitutions selected from the group consisting of S3T, V4I, V193M and V199I.

Mutations

SEQ ID NO:1 Similarity: 91% V199I V

SEQ ID NO:1 Similarity: 91% V199I V

Abstract differs

US20150017707 A1  
Publication: 2015-01-15  
Applicant: BASF SE

EP2809763 B1 **Granted**  
Publication: 2017-01-04  
Applicant: BASF SE

Patent family members without mutations at this position: WO2013113619 A1

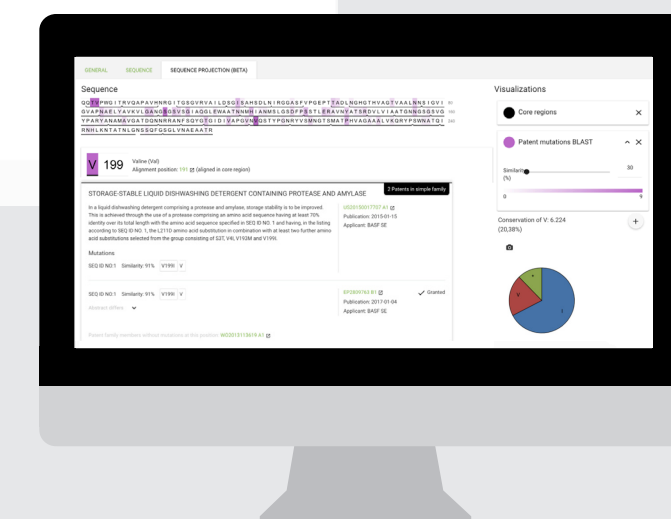
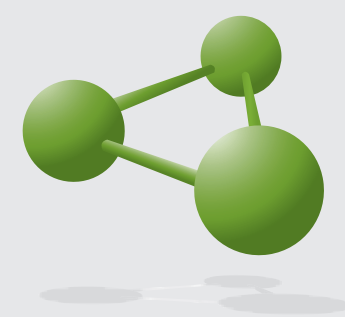
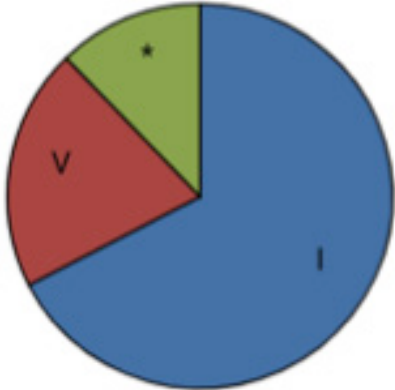
Visualizations

Core regions

Patent mutations BLAST

Similarity (%) 30

Conservation of V: 6.224 (20,38%)



**For more information visit our website:**  
**[www.bio-product.nl](http://www.bio-product.nl)**

**or request information via:**  
**[info@bio-product.nl](mailto:info@bio-product.nl)**

